

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)
)
Salvatore Albani)
)
Serial No: Not yet assigned)
)
Filed: Herewith)
)
For: METHODS FOR ISOLATION,)
QUANTIFICATION, CHARACTERIZATION)
AND MODULATION OF ANTIGEN-SPECIFIC T)
CELLS)

SUBMISSION OF SEQUENCE LISTING

Commissioner for Patents
Washington, D.C. 20231

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Respectfully submitted,

Brobeck, Phleger & Harrison LLP

Dated: 1/19/07

By 

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SEQUENCE LISTING

<110> Albani, Salvatore

<120> METHODS FOR ISOLATION, QUANTIFICATION,
CHARACTERIZATION AND MODULATION OF
ANTIGEN-SPECIFIC T CELLS

<130> 031544.0004.CIP

<140> NOT YET ASSIGNED

<141> 2001-01-09

<150> 60/105,018

<151> 1998-10-20

<150> 09/421,506

<151> 1999-10-19

<150> PCT/US99/2466

<151> 1999-10-19

<160> 24

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<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Synthesized peptide derived from third hyper V
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<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from boe I protein
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031544.0004.CIP

<210> 3
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<220>
 <223> Synthesized peptide derived from the hemophilus
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<210> 4
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the TCR receptor
 gene of Mus musculus

<400> 4
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 Arg Leu
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<220>
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<210> 6
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<220>
 <223> Synthesized peptide derived from the influenza virus

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00569260

<210> 7
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide totally artificial

<220>
 <223> Xaa in position 2 stands for cyclohexylalanine

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<210> 8
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<220>
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<210> 9
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<220>
 <223> Synthesized peptide derived from the ovalbumin
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<210> 10
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 <212> PRT
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<220>
 <223> dnaJpl heat shock protein

<400> 10
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00756983-01001

<210> 11
 <211> 15
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 <213> Homo sapiens

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 <212> PRT
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<400> 12
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<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
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<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

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 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
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<210> 15
 <211> 313
 <212> PRT
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<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 15
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 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
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gaagtgaaag	aagtggcaac	gctgtcctgt	ggtcacaatg	tttctgttga	agagctggca	180
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atgaatatat	ggccccagta	caagaaccgg	accatctttg	atatcactaa	taacctctcc	300
attgtgatcc	tggtctcgcg	cccatctgac	gagggcacat	acgagtgtgt	tgttctgaag	360
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gacttcccta	cacctagtat	atctgacttt	gaaattccaa	cttctaatat	tagaaggata	480
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<211> 1056

<212> DNA

<213> Artificial Sequence

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<223> Fusion constructs with human and bacterial sequences

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ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
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aagaagatga gtgttttgc aagaaccaag aattcaacta tcgagtatga tggattatg 540
cagaaatctc aagataatgt cacagaactg tacgacgtt ccatcagctt gtctgtttca 600
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ccaggtagtc aacatataga ttcacaaaaa aaagcgattg aaaggatgaa ggataccctg 960
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cctcatgcga ttgccgcaat tagtatggca aattaa 1056

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 18

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20           25           30
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
35           40           45
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50           55           60
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
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Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
85           90           95

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<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence
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<210> 20
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptides

<400> 20
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 Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
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<210> 21
 <211> 1095
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 21
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 cctgaccaat caggcgagtt tatgtttgac tttgatggtg atgagatttt ccatgtggat 180
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 <211> 364
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 22
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 20 25 30

F05070" E9695460

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
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<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 23

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 aaacatgagt gtcatttctt caacgggacg gagcggtgac ggttcctgga cagatacttc 180
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0975693.040504

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<210> 24

<211> 285

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<213> Artificial Sequence

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<223> Fusion constructs with human and bacterial sequences

<400> 24

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          35          40          45
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
          50          55          60
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
65          70          75          80
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
          85          90          95
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
          100          105          110
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
          115          120          125
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
          130          135          140
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145          150          155          160
Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
          165          170          175
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
          180          185          190
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
          195          200          205
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
          210          215          220
Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
225          230          235          240
Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
          245          250          255
Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
          260          265          270
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
          275          280          285

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